

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: March 9, 2002, 00:48:46 ; Search time 2351.15 Seconds
(Without alignments) 175.416 Million cell updates/sec

Title: US-09-851-670-19

Sequence: 1 gctgcatctgtatccctcttgc 25

Scoring table: IDENTITY-NUC
Gapop 10.0 , Gapext 1.0

Searched: 1472140 segs, 8248589755 residues

Total number of hits satisfying chosen parameters: 586436

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenBank:*

1: gb.ba:*
2: gb.htg:*
3: gb.in:*
4: gb.om:*
5: gb.ov:*
6: gb.pat:*
7: gb.ph:*
8: gb.pl:*
9: gb.pr:*
10: gb.ro:*
11: gb.sts:*
12: gb.sy:*
13: gb.un:*
14: gb.vi:*
15: em.ba:*
16: em.fun:*
17: em.hum:*
18: em.in:*
19: em.om:*
20: em.or:*
21: em.ov:*
22: em.pat:*
23: em.ph:*
24: em.pl:*
25: em.ro:*
26: em.sts:*
27: em.sy:*
28: em.un:*
29: em.vi:*
30: em.htgo.hum:*
31: em.htgo.inv:*
32: em.htgo.rod:*
33: em.htg.hum:*
34: em.htg.inv:*
35: em.htg.rod:*
36: em.htg.other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15.4	61.6	41	9	S80780
2	15	60.0	60	6	E22161
3	14.6	58.4	22	6	AX081807
4	14.6	58.4	22	6	AX081905
5	14.2	56.8	51	6	AX157013
6	14.2	56.8	51	6	AX157014
7	14	56.0	23	6	AX004585
8	13.8	55.2	47	6	A41406
9	13.8	55.2	47	6	AR091266
10	13.8	55.2	60	6	AR138815
11	13.6	54.4	51	6	AX160625
12	13.6	54.4	51	6	AX160626
13	13.6	54.4	56	3	AF039629
14	13.4	53.6	32	6	A69296
15	13.4	53.6	32	6	A71973
16	13.4	53.6	32	6	AR147161
17	13.4	53.6	39	9	HSTCARB29
18	13.2	52.8	20	12	AB068982
19	13.2	52.8	24	6	E36319
20	13.2	52.8	25	6	E14083
21	13.2	52.8	36	6	A47908
22	13.2	52.8	36	6	AR028431
23	13.2	52.8	39	6	A14923
24	13.2	52.8	51	6	A14924
25	13.2	52.8	51	6	AX158056
26	13	52.0	26	6	AR153330
27	13	52.0	26	6	AX045398
28	13	52.0	26	6	AX045445
29	13	52.0	26	6	AX045743
30	13	52.0	26	6	AX045807
31	13	52.0	30	6	I90037
32	13	52.0	40	6	I18869
33	13	52.0	40	6	I36795
34	13	52.0	40	6	I55999
35	13	52.0	41	6	A62582
36	13	52.0	46	6	AR117906
37	13	52.0	50	6	AX093099
38	12.8	51.2	30	6	AX046577
39	12.8	51.2	36	9	HS010875
40	12.8	51.2	40	6	I04762
41	12.8	51.2	41	6	AR147684
42	12.8	51.2	44	6	AR147685
43	12.8	51.2	51	6	AX159110
44	12.8	51.2	51	6	AX165777
45	12.8	51.2	53	6	I68860

ALIGNMENTS

RESULT	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	MEDLINE	REMARK
1	S80780/c	gamma delta T cell antigen receptor delta-chain [V delta 1-J delta 1 junction] [human, skin lesion, Genomic, 41 nt].	S80780			S80780.1 GI:244968	human skin lesion.	41 bp	DNA	PRI	07-MAY-1993		
							Homo sapiens						
							Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;						
							Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.						
							1 (bases 1 to 41)						
							Uyemura,K., Klotz,J., Plimetz,C., Ohmen,J., Wang,X.H., Ho,C.,						
							Hoffman,W.L. and Modlin,R.L.						
							Microclonal clonality of gamma delta T cells in human						
							Leishmaniasis lesions						
							J. Immunol. 148 (4), 1205-1211 (1992)						
							GenBank staff at the National Library of Medicine created this						

RESULT 3

ACCESSION

[illegible]

VERSION	AR004585.1	GI:3965464
KEYWORDS	Unknown.	
SOURCE	Unknown.	
ORGANISM	Unclassified.	
REFERENCE	1 (bases 1 to 23)	
AUTHORS	Jensen,M.Anton.	
TITLE	Genetic markers and methods for the detection of escherichia coli serotype-0157:H7	
JOURNAL	Patent; US 5747257-A 8 05-MAY-1998;	
FEATURES	Location/Qualifiers	
source	1..23	
BASE COUNT	5 a /organism="unknown"	8 t
ORIGIN	5 a 6 c 4 g	
Query Match	56.0%; Score 14; DB 6; Length 23;	
Best Local Similarity	77.3%; Pred. No. 6.8e+04;	
Matches	17; Conservative 0; Mismatches 5; Indels 0; Gaps 0.	
OY	2 ctccgactctgtatcccttc tt 23 	
Dd	1 CTCATCTGTAGAGCCGCTACTT 22	
RESULT	8	
LOCUS	A41406 47 bp DNA	PAT 05-MAR-1997
DEFINITION	Sequence 6 from Patent WO9426886.	
ACCESSION	A41406	
VERSION	A41406.1 GI:2297122	
KEYWORDS	unidentified.	
SOURCE	unidentified	
ORGANISM	unclassified.	
REFERENCE	1 (bases 1 to 47)	
AUTHORS	Felici,F., Luzzago,A., Nicosia,A., Monaci,P. and Cortese,R.	
TITLE	PROCESS FOR THE PREPARATION OF IMMUNOGENS OR DIAGNOSTIC REAGENTS, AND IMMUNOGENS OR DIAGNOSTIC REAGENTS THEREBY OBTAINABLE	
JOURNAL	Patent; WO 9426886-A 6 24-NOV-1994;	
COMMENT	ISTITUTO DI RICERCHE DI BIOLOG (IT) Other publication AU 6806994 941212 Other publication CA 2160486 941124 Other publication BR 9406595 960102 other publication JP 8506493T 960716. Location/Qualifiers	
FEATURES	1..47	
source	/organism="unidentified"	
BASE COUNT	4 a /db_xref="taxon:32644"	15 t
ORIGIN	15 c 13 g	
Query Match	55.2%; Score 13.8; DB 6; Length 47;	
Best Local Similarity	88.2%; Pred. No. 7.8e+04;	
Matches	15; Conservative 0; Mismatches 2; Indels 0; Gaps 0.	
OY	7 tctgtgatcccttctt tt 23 	
Dd	5 TCTGGCGTCCTCTTT 21	
RESULT	9	
LOCUS	AR091266 47 bp DNA	PAT 07-SEP-2000
DEFINITION	Sequence 6 from patent US 5994083.	
ACCESSION	AR091266	
VERSION	AR091266.1 GI:10018021	
KEYWORDS	Unknown.	
SOURCE	Unknown.	
ORGANISM	Unclassified.	

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REFERENCE 1 (bases 1 to 47)
AUTHORS Felici,F., Luzzago,A., Monaci,P., Nicotia,A. and Cortese,R.
TITLE Process for the preparation of immunogens or diagnostic reagents,
JOURNAL and immunogens of diagnostic reagents thereby obtainable
FEATURES Patent: US 5994083-A 6 30-NOV-1999;
SOURCE Location/Qualifiers
1..47
BASE COUNT 4 a 15 c 13 g 15 t
ORIGIN

Query Match
Best Local Similarity 55.2%; Score 13.8; DB 6; Length 47;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 tctgtgacccctctt 23
Db 5 TCTGCGTCCCTCTT 21

RESULT 10
ARI38815 LOCUS ARI38815 60 bp DNA PAT 16-JUN-2001
DEFINITION Sequence 4 from patent US 6200758.
ACCESSION ARI38815
VERSION ARI38815.1 GI:14481160
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 60)
AUTHORS Richardson,M,Ann.
TITLE Phenylalanine hydroxylase gene variants, and amino acid and pterin
JOURNAL homeostasis, in the definition, detection, treatment and prevention
FEATURES Patent: US 6200758-A 4 13-MAR-2001;
SOURCE Location/Qualifiers
1..60
BASE COUNT 1 a 33 c 14 g 12 t
ORIGIN

Query Match
Best Local Similarity 55.2%; Score 13.8; DB 6; Length 60;
Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 gtcgacgtgacccctcttgc 25
Db 36 GCCCGTCTGTTCTTTTCATTCG 60

RESULT 11
AXI60625 LOCUS AXI60625 51 bp DNA PAT 22-JUN-2001
DEFINITION Sequence 3953 from Patent WO0140521.
ACCESSION AXI60625
VERSION AXI60625.1 GI:14541956
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
TITLE 1 (bases 1 to 51)
AUTHORS Shimkets,R.A. and Leach,M.
JOURNAL Nucleic acids containing single nucleotide polymorphisms and
FEATURES Patent: WO 0140521-A 3953 07-JUN-2001;
SOURCE Location/Qualifiers
1..51
/organism="Homo sapiens"

misc.feature
/db_xref="taxon:9606"
26
/note="1 of 2 allelic variants (3954 is other entry)
Accession number cg43925525"
BASE COUNT 9 a 14 c 9 g 19 t
ORIGIN

Query Match
Best Local Similarity 54.4%; Score 13.6; DB 6; Length 51;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 tgcgtgacccctctt 22
Db 22 TGGACTGTGTCCGTTCTT 41

RESULT 12
AXI60626 LOCUS AXI60626 51 bp DNA PAT 22-JUN-2001
DEFINITION Sequence 3954 from Patent WO0140521.
ACCESSION AXI60626
VERSION AXI60626.1 GI:14541957
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
TITLE 1 (bases 1 to 51)
AUTHORS Shimkets,R.A. and Leach,M.
JOURNAL Nucleic acids containing single nucleotide polymorphisms and
FEATURES Patent: WO 0140521-A 3954 07-JUN-2001;
SOURCE Location/Qualifiers
1..51
BASE COUNT 10 a 13 c 9 g 19 t
ORIGIN

misc.feature
/db_xref="taxon:9606"
26
/note="2 of 2 allelic variants (3953 is other entry)
Accession number cg43925525"
BASE COUNT 10 a 13 c 9 g 19 t
ORIGIN

Query Match
Best Local Similarity 54.4%; Score 13.6; DB 6; Length 51;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 tgcgtgacccctctt 22
Db 22 TGGACTGTGTCCGTTCTT 41

RESULT 13
AF039629 LOCUS AF039629 56 bp DNA INV 23-MAR-1998
DEFINITION Drosophila hydei xanthine dehydrogenase gene, intron II.
ACCESSION AF039629
VERSION AF039629.1 GI:2981344
KEYWORDS
SOURCE Drosophila hydei.
ORGANISM Drosophila hydei
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
REFERENCE Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
TITLE 1 (bases 1 to 56)
AUTHORS Tarrío,R., Rodríguez-Trelles,F. and Ayala,F.J.
JOURNAL New drosophila introns originate by duplication
FEATURES Proc. Natl. Acad. Sci. U.S.A. 95 (4), 1658-1662 (1998)
SOURCE 98132647
REFERENCE 2 (bases 1 to 56)
AUTHORS Tarrío,R., Rodríguez-Trelles,F. and Ayala,F.J.

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